STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
   ERROR REPORT

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Application Serial Number: _10/516,992_

Source: _PCT/10_

Date Processed by STIC: _1/23/06_

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1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/24/05

PCT

RAW SEQUENCE LISTING   DATE: 01/23/2006
PATENT APPLICATION: US/10/516,992   TIME: 09:45:13

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

```
 3 <110> APPLICANT: Galloway, Susan May
 4        Davis, George Henry
 5        Gregan, Scott Michael
 6        Hanrahan, James Patrick
 7        Juengel, Jennifer Lee
 8        McNatty, Kenneth Pattrick
 9        Mulsant, Philippe
10        Powell, Richard Patrick
13 <120> TITLE OF INVENTION: NEW GDF-9 AND GDF-9B (BMP-15) SEQUENCES FOR
14        ALTERING MAMMALIAN OVARIAN FUNCTION AND OVULATION RATE
16 <130> FILE REFERENCE: AJPARK27.001APC
18 <140> CURRENT APPLICATION NUMBER: US 10/516992
19 <141> CURRENT FILING DATE: 2004-11-30
21 <150> PRIOR APPLICATION NUMBER: PCT/NZ03/00109
22 <151> PRIOR FILING DATE: 2003-05-30
24 <160> NUMBER OF SEQ ID NOS: 18
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1879
30 <212> TYPE: DNA
31 <213> ORGANISM: Ovis aries
W--> 32 <220> FEATURE:
33 <221> NAME/KEY: 5'UTR
34 <222> LOCATION: (1)..(121)
W--> 35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (122)..(124)
38 <223> OTHER INFORMATION: atg start codon.
W--> 39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (122)..(518)
W--> 42 <220> FEATURE:
43 <221> NAME/KEY: CDS
W--> 44 <220> FEATURE:
45 <221> NAME/KEY: Intron
46 <222> LOCATION: (519)..(838)
   47 <223> OTHER INFORMATION: n at 709 represents remainder of approx 900 bp unsequenced of
the approx
   48        1.1 kb intron
W--> 49 <220> FEATURE:
50 <221> NAME/KEY: mat_peptide
51 <222> LOCATION: (1396)..()
W--> 52 <220> FEATURE:
53 <221> NAME/KEY: misc_feature
```

Handwritten annotations: 1878 (see below)

Handwritten annotation: pp 1-2, 4, 6

Stamp: Does Not Comply — Corrected Diskette Needed

Handwritten annotation: "n" can only represent a single nucleotide. (Per Sequence Rules) Suggestion: delete the "n" and just state that approx 900 base pairs were ↙ (add this)

Handwritten annotation: This type of error appears in Seqs 7 and 13

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Input Set : A:\PTO.RJ.txt
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delete — already on p. 1

```
54 <222> LOCATION: (709)..()
55 <223> OTHER INFORMATION: n represents approximately 900 bp of unsequenced intron.
W--> 56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (1801)..(1803)
59 <223> OTHER INFORMATION: taa stop codon.
W--> 60 <220> FEATURE:
61 <221> NAME/KEY: 3'UTR
62 <222> LOCATION: (1804)..(1879)
W--> 63 <220> FEATURE:
64 <221> NAME/KEY: mutation
65 <222> LOCATION: (1624)..(1626)
66 <223> OTHER INFORMATION: c to t at 1625 in [787] sheep changing tct serine codon to
ttt
67         phenylalanine
69 <400> SEQUENCE: 1
70 gaattgaacc tagcccaccc acacacctaa agtttattta agagaccaac cgaggctctt        60
72 cctggttttt aggaagaaga ctggtatggg gaaatgtgtt ccttgctaat tcttccaagc       120
74 c atg gcg ctt ccc  aac aaa ttc ttc ctt  tgg ttt tgc tgc ttt  gcc       166
76   Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
77              -315                -310                -305
79 tgg ctc tgt ttt  cct att agc ctt gat  tct ctg cct tct agg  gga       211
80 Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
81              -300                -295                -290
83 gaa gct cag att  gta gct agg act gcg  ttg gaa tct gag gct  gag       256
84 Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
85              -285                -280                -275
87 act tgg tcc ttg  ctg aac cat tta ggt  ggg aga cac aga cct  ggt       301
88 Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
89              -270                -265                -260
91 ctc ctt tcc cct  ctc tta gag gtt ctg  tat gat ggg cac ggg  gaa       346
92 Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
93              -255                -250                -245
95 ccc ccc agg ctg  cag cca gat gac aga  gct ttg cgc tac atg  aag       391
96 Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
97              -240                -235                -230
99 agg ctc tat aag  gca tac gct acc aag  gag ggg acc cct aaa  tcc       436
100 Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
101              -225                -220                -215
103 aac aga cgc cac  ctc tac aac act gtt  cgg ctc ttc acc ccc  tgt       481
104 Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
105              -210                -205                -200
107 gct cag cac aag  cag gct cct ggg gac  ctg gcg gca g gtgtgtagga        528
108 Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala
109              -195                -190
111 gcagattggt taatgggtgg agggaagaag aaagaccttt ttgcatttca gttacataaa       588
113 ggagttggcc ctgctccttg acttgcattt tactttgcat ggtactcaat atccaaacaa       648
115 acctggtgct tgatcttact tactgtttat tcctaatggc ctcatgggtt gatgtaggct       708
W--> 117 natcccaccc tgacgtttaa ggcttgagaa tgtggggaga aaagggacag aagcacattc       768
119 tgaggtactg attccttgat ttgacttcct gttacatatg gcattactgt tggattgttt       828
```

```
121 ttcttctcag ga  acc ttt cca tca gtg gat  ctg ctg ttt aac ctg  gat    876
122            Gly Thr Phe Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp
125                -185                -180                -175
127 cgt gtt act gtt  gtg gaa cat tta ttc  aag tca gtc ttg ctg  tat    921
128 Arg Val Thr Val  Val Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr
129             -170                -165                -160
131 act ttc aac aac  tcc att tct ttt ccc  ttt cct gtt aaa tgt  ata    966
132 Thr Phe Asn Asn  Ser Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile
133             -155                -150                -145
135 tgc aac ctg gtg  ata aaa gag cca gag  ttt tct agc aag act  ctc   1011
136 Cys Asn Leu Val  Ile Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu
137             -140                -135                -130
139 cct aga gct cca  tac tca ttt acc tat  aac tca cag ttt gaa  ttt   1056
140 Pro Arg Ala Pro  Tyr Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe
141             -125                -120                -115
143 aga aag aaa tac  aaa tgg atg gag att  gat gtg acg gct cct  ctt   1101
144 Arg Lys Lys Tyr  Lys Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu
145             -110                -105                -100
147 gag cct ctg gtg gcc tcc cac aag agg aat att cac atg tct gta aat   1149
148 Glu Pro Leu Val Ala Ser His Lys Arg Asn Ile His Met Ser Val Asn
149             -95                -90                -85
151 ttt aca tgt gcg gaa gac cag ctg cag cat cct tca gcg cgg gac agc   1197
152 Phe Thr Cys Ala Glu Asp Gln Leu Gln His Pro Ser Ala Arg Asp Ser
153          -80                -75                -70
155 ctg ttt aac atg act ctt ctc gta gcg ccc tca ctg ctt ttg tat ctg   1245
156 Leu Phe Asn Met Thr Leu Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu
157     -65                -60                -55
159 aac gac aca agt gct cag gct ttt cac agg tgg cat tcc ctc cac cct   1293
160 Asn Asp Thr Ser Ala Gln Ala Phe His Arg Trp His Ser Leu His Pro
161 -50                -45                -40                -35
163 aaa agg aag cct tca cag ggt cct gac cag aag aga ggg cta tct gcc   1341
164 Lys Arg Lys Pro Ser Gln Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala
165             -30                -25                -20
167 tac ccc gtg gga gaa gaa gct gct gag ggt gta aga tcg tcc cgt cac   1389
168 Tyr Pro Val Gly Glu Glu Ala Ala Glu Gly Val Arg Ser Ser Arg His
169             -15                -10                -5
171 cgc aga gac cag gag agt gcc agc tct gaa ttg aag aag cct ctg gtt   1437
172 Arg Arg Asp Gln Glu Ser Ala Ser Ser Glu Leu Lys Lys Pro Leu Val
173   -1  1                5                10
176 cca gct tca gtc aat ctg agt gaa tac ttc aaa cag ttt ctt ttt ccc   1485
177 Pro Ala Ser Val Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro
178 15                20                25                30
180 cag aat gaa tgt gag ctc cat gac ttt aga ctt agc ttt agt cag ctg   1533
181 Gln Asn Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu
182         35                40                45
184 aag tgg gac aac tgg att gtg gcc cca cac aaa tac aac cct cga tac   1581
185 Lys Trp Asp Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr
186         50                55                60
188 tgt aaa ggg gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg   1629
```

```
                 RAW SEQUENCE LISTING              DATE: 01/23/2006
                 PATENT APPLICATION:  US/10/516,992   TIME: 09:45:13

                 Input Set : A:\PTO.RJ.txt
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```

```
189 Cys Lys Gly Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro
190          65                    70                    75
192 gtt cac acc atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca      1677
193 Val His Thr Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser
194          80                    85                    90
196 gtg cca aga cca tcc tgt gta cct gcc aag tat agc cct ttg agt gtt      1725
197 Val Pro Arg Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val
198 95                   100                   105                   110
200 ttg gcc atc gag cct gat ggc tca atc gct tat aaa gaa tat gaa gat      1773
201 Leu Ala Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp
202                  115                   120                   125
204 atg ata gcc act aag tgt acc tgt cgt taacagactc ctgtcaagta           1820
205 Met Ile Ala Thr Lys Cys Thr Cys Arg
206          130                   135
208 aaaccatgag tgtcctggcc agtgtaaatg ccgcgcccct gtctatgcct ttgggagga    1879
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 453
213 <212> TYPE: PRT
214 <213> ORGANISM: Ovis aries
```
delete these - they do not apply to a peptide sequence (handwritten)
```
W-->   215 <220> FEATURE:
       216 <221> NAME/KEY: misc_feature
       217 <222> LOCATION: (122)..(124)
       218 <223> OTHER INFORMATION: atg start codon.
W-->   219 <220> FEATURE:
       220 <221> NAME/KEY: misc_feature
       221 <222> LOCATION: (709)..()
       222 <223> OTHER INFORMATION: n represents approximately 900 bp of unsequenced intron
W-->   223 <220> FEATURE:
       224 <221> NAME/KEY: misc_feature
       225 <222> LOCATION: (1801)..(1803)
       226 <223> OTHER INFORMATION: taa stop codon.
```
same type of error in subsequent peptide sequences, too. (handwritten)
```
       229 <400> SEQUENCE: 2
       231 Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
       232              -315                 -310              -305
       235 Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
       236              -300                 -295              -290
       239 Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
       240              -285                 -280              -275
       243 Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
       244              -270                 -265              -260
       247 Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
       248              -255                 -250              -245
       251 Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
       252              -240                 -235              -230
       255 Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
       256              -225                 -220              -215
       259 Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
       260              -210                 -205              -200
       263 Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
```

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

```
264        ·        -195              -190               -185
267 Pro Ser Val Asp Leu Leu Phe Asn Leu Asp Arg Val Thr Val Val
268            -180              -175              -170
271 Glu His Leu Phe Lys Ser Val Leu Leu Tyr Thr Phe Asn Asn Ser
272            -165              -160              -155
275 Ile Ser Phe Pro Phe Pro Val Lys Cys Ile Cys Asn Leu Val Ile
276            -150              -145              -140
279 Lys Glu Pro Glu Phe Ser Ser Lys Thr Leu Pro Arg Ala Pro Tyr
280            -135              -130              -125
283 Ser Phe Thr Tyr Asn Ser Gln Phe Glu Phe Arg Lys Lys Tyr Lys
284            -120              -115              -110
287 Trp Met Glu Ile Asp Val Thr Ala Pro Leu Glu Pro Leu Val Ala Ser
288            -105              -100              -95
291 His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
292            -90               -85               -80
295 Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
296       -75  .              -70               -65
299 Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
300 -60              -55               -50               -45
303 Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
304            -40               -35               -30
307 Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
308            -25               -20               -15
311 Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
312            -10               -5               -1  1
315 Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
316 5               10                15                20
319 Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
320            25                30                35
323 His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
324            40                45                50
327 Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
328    ·       55                60                65
331 Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
332    70                75                80
335 Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
336 85               90                95                100
339 Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
340            105               110               115
343 Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
344            120               125               130
347 Thr Cys Arg
348       135
352 <210> SEQ ID NO: 3
353 <211> LENGTH: 1362
354 <212> TYPE: DNA
355 <213> ORGANISM: Ovis aries
356 <220> FEATURE:
357 <221> NAME/KEY: misc_feature
```

W--> 356

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/23/2006
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Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

Please Note: ·
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 709
Seq#:7; N Pos. 685
Seq#:13; N Pos. 685

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 47
Seq#:3; Line(s) 369
Seq#:15; Line(s) 1437

VERIFICATION SUMMARY   DATE: 01/23/2006
PATENT APPLICATION: **US/10/516,992**   TIME: 09:45:14

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

```
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <220> field identifier
L:39 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:63 M:283 W: Missing Blank Line separator, <220> field identifier
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:708
L:215 M:283 W: Missing Blank Line separator, <220> field identifier
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:356 M:283 W: Missing Blank Line separator, <220> field identifier
L:360 M:283 W: Missing Blank Line separator, <220> field identifier
L:363 M:283 W: Missing Blank Line separator, <220> field identifier
L:366 M:283 W: Missing Blank Line separator, <220> field identifier
L:370 M:283 W: Missing Blank Line separator, <220> field identifier
L:503 M:283 W: Missing Blank Line separator, <220> field identifier
L:507 M:283 W: Missing Blank Line separator, <220> field identifier
L:638 M:283 W: Missing Blank Line separator, <220> field identifier
L:641 M:283 W: Missing Blank Line separator, <220> field identifier
L:691 M:283 W: Missing Blank Line separator, <220> field identifier
L:694 M:283 W: Missing Blank Line separator, <220> field identifier
L:698 M:283 W: Missing Blank Line separator, <220> field identifier
L:701 M:283 W: Missing Blank Line separator, <220> field identifier
L:704 M:283 W: Missing Blank Line separator, <220> field identifier
L:708 M:283 W: Missing Blank Line separator, <220> field identifier
L:712 M:283 W: Missing Blank Line separator, <220> field identifier
L:716 M:283 W: Missing Blank Line separator, <220> field identifier
L:720 M:283 W: Missing Blank Line separator, <220> field identifier
L:723 M:283 W: Missing Blank Line separator, <220> field identifier
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:637
L:830 M:283 W: Missing Blank Line separator, <220> field identifier
L:834 M:283 W: Missing Blank Line separator, <220> field identifier
L:838 M:283 W: Missing Blank Line separator, <220> field identifier
L:842 M:283 W: Missing Blank Line separator, <220> field identifier
L:913 M:283 W: Missing Blank Line separator, <220> field identifier
L:917 M:283 W: Missing Blank Line separator, <220> field identifier
L:921 M:283 W: Missing Blank Line separator, <220> field identifier
L:924 M:283 W: Missing Blank Line separator, <220> field identifier
L:928 M:283 W: Missing Blank Line separator, <220> field identifier
L:1018 M:283 W: Missing Blank Line separator, <220> field identifier
L:1022 M:283 W: Missing Blank Line separator, <220> field identifier
L:1026 M:283 W: Missing Blank Line separator, <220> field identifier
L:1098 M:283 W: Missing Blank Line separator, <220> field identifier
L:1101 M:283 W: Missing Blank Line separator, <220> field identifier
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VERIFICATION SUMMARY   DATE: 01/23/2006
PATENT APPLICATION: **US/10/516,992**   TIME: 09:45:14

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\01232006\J516992.raw**

```
L:1138 M:283 W: Missing Blank Line separator, <220> field identifier
L:1141 M:283 W: Missing Blank Line separator, <220> field identifier
L:1145 M:283 W: Missing Blank Line separator, <220> field identifier
L:1148 M:283 W: Missing Blank Line separator, <220> field identifier
L:1151 M:283 W: Missing Blank Line separator, <220> field identifier
L:1155 M:283 W: Missing Blank Line separator, <220> field identifier
L:1158 M:283 W: Missing Blank Line separator, <220> field identifier
L:1162 M:283 W: Missing Blank Line separator, <220> field identifier
L:1166 M:283 W: Missing Blank Line separator, <220> field identifier
L:1169 M:283 W: Missing Blank Line separator, <220> field identifier
L:1219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:667
L:1306 M:283 W: Missing Blank Line separator, <220> field identifier
L:1310 M:283 W: Missing Blank Line separator, <220> field identifier
L:1314 M:283 W: Missing Blank Line separator, <220> field identifier
L:1430 M:283 W: Missing Blank Line separator, <220> field identifier
L:1434 M:283 W: Missing Blank Line separator, <220> field identifier
L:1439 M:283 W: Missing Blank Line separator, <220> field identifier
L:1442 M:283 W: Missing Blank Line separator, <220> field identifier
L:1445 M:283 W: Missing Blank Line separator, <220> field identifier
L:1561 M:283 W: Missing Blank Line separator, <220> field identifier
L:1565 M:283 W: Missing Blank Line separator, <220> field identifier
L:1680 M:283 W: Missing Blank Line separator, <220> field identifier
L:1683 M:283 W: Missing Blank Line separator, <220> field identifier
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